

MitoBench: An interactive visual workbench for population genetics on mitochondrial DNA



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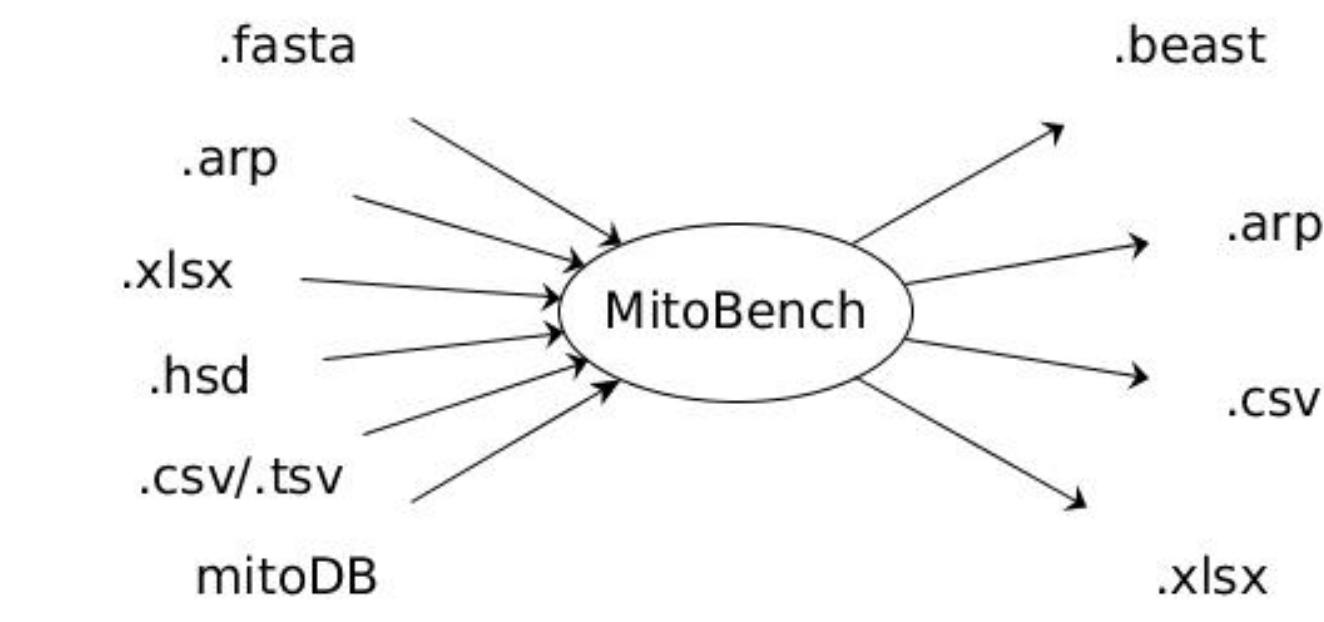
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Introduction

Despite the availability of modern next generation sequencing technologies and therefore nuclear human genomes, the sequencing and analysis of mitochondrial DNA (mtDNA) is still common. Especially in the research field of ancient DNA and the context of population genetics, mtDNA is often the only proxy available to study extinct populations and their relationship with modern populations. As a consequence, many population genetic studies rely on the analysis of mtDNA. A plethora of methods for the analysis of mtDNA exist, that address questions in population genetics, phylogeny and others. However, these tools typically rely on different file formats and often require manual interaction with the data for downstream analysis. Ultimately, these steps can be cumbersome, especially for non-bioinformaticians, resulting in an increased risk of errors during the analysis. To tackle these issues, we present MitoBench, a workbench to interactively analyze and visualize mitochondrial genomes with a focus on population genetics. The graphical user interface is kept simple, to accommodate even users without further prior knowledge on computational methods. Furthermore, it shows additional information such as metadata and statistics. Currently, MitoBench offers automatic file conversion tools to connect the workbench with existing analysis methods such as BEAST, Arlequin and others.

MitoBench

Data import and export



Data representation

User table									
ID	MTSequence	Haplogroup	Time Period	continent	country	country_region	culture_type	dating_lower	
JK2880	GATCA...	T1a2	Pre-Ptolemaic Period	Africa	Egypt	Beni Suef	Ancient	469	
egypt.5A129	GATCA...	X1c	Egypt Modern	Africa	Egypt	Other	Modern	2015	
egypt.6A08	GATCA...	H3w	Egypt Modern	Africa	Egypt	Other	Modern	2015	
egyp3305866	GATCA...	L3Q2a1	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015	
egypt.6A03	GATCA...	R0a3	Egypt Modern	Africa	Egypt	Other	Modern	2015	
egyp3305863	GATCA...	M1a5	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015	
egyp3305862	GATCA...	R0a2	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015	
egyp3306038	GATCA...	R0a2b	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015	
egyp3306032	GATCA...	L0P2b	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015	
egyp3306031	GATCA...	L3b2	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015	
egyp3306030	GATCA...	L2a1d1	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015	
egypt.7A6139	GATCA...	R0b	Egypt Modern	Africa	Egypt	Other	Modern	2015	
JK2879	GATCA...	U3b	Roman Period	Africa	Egypt	Beni Suef	Ancient	2015	
JK2878	GATCA...	T1a7	Ptolemaic Period	Africa	Egypt	Beni Suef	Ancient	235	
egypt.8A134	GATCA...	H20c	Egypt Modern	Africa	Egypt	Other	Modern	2015	

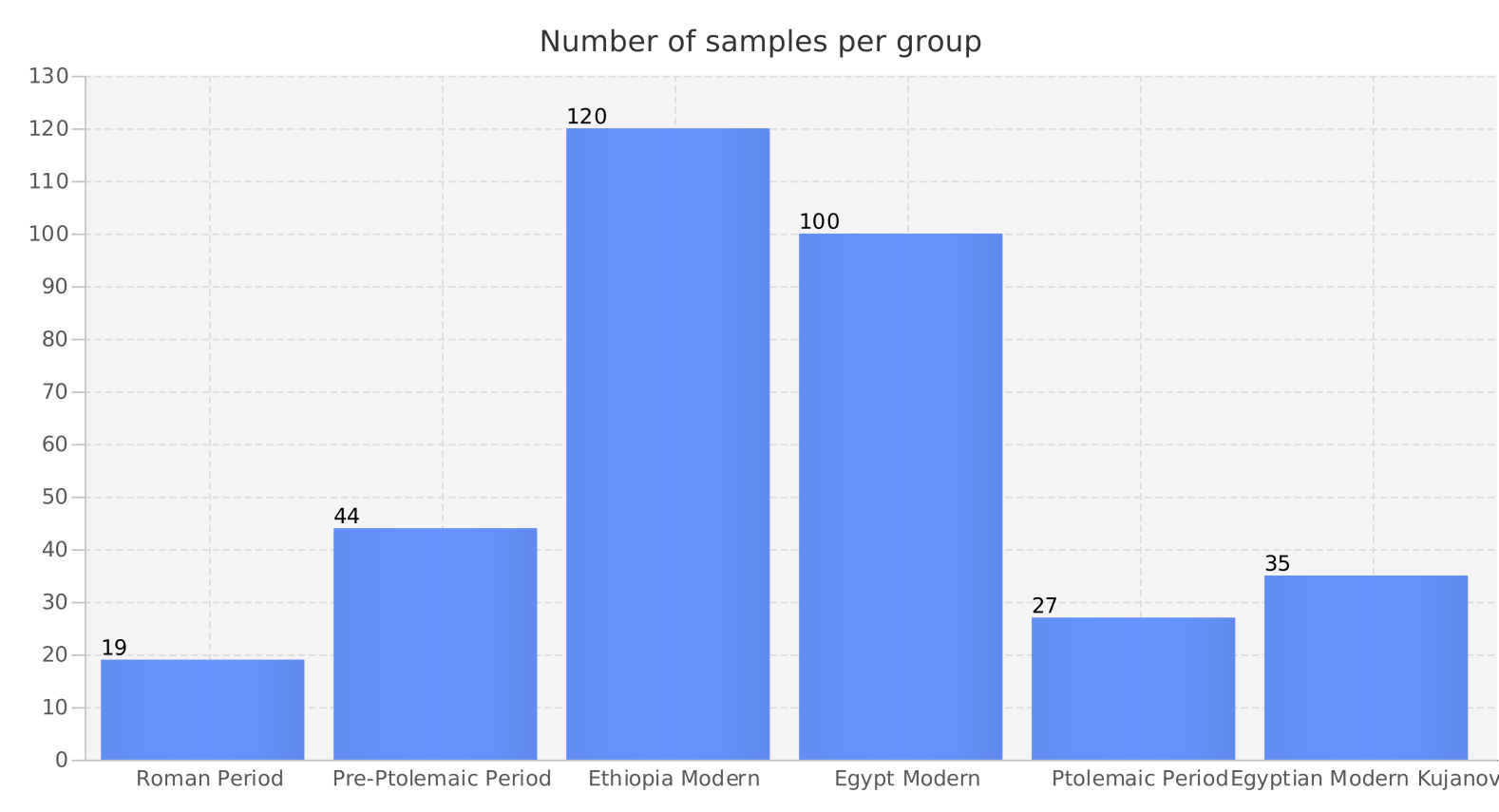
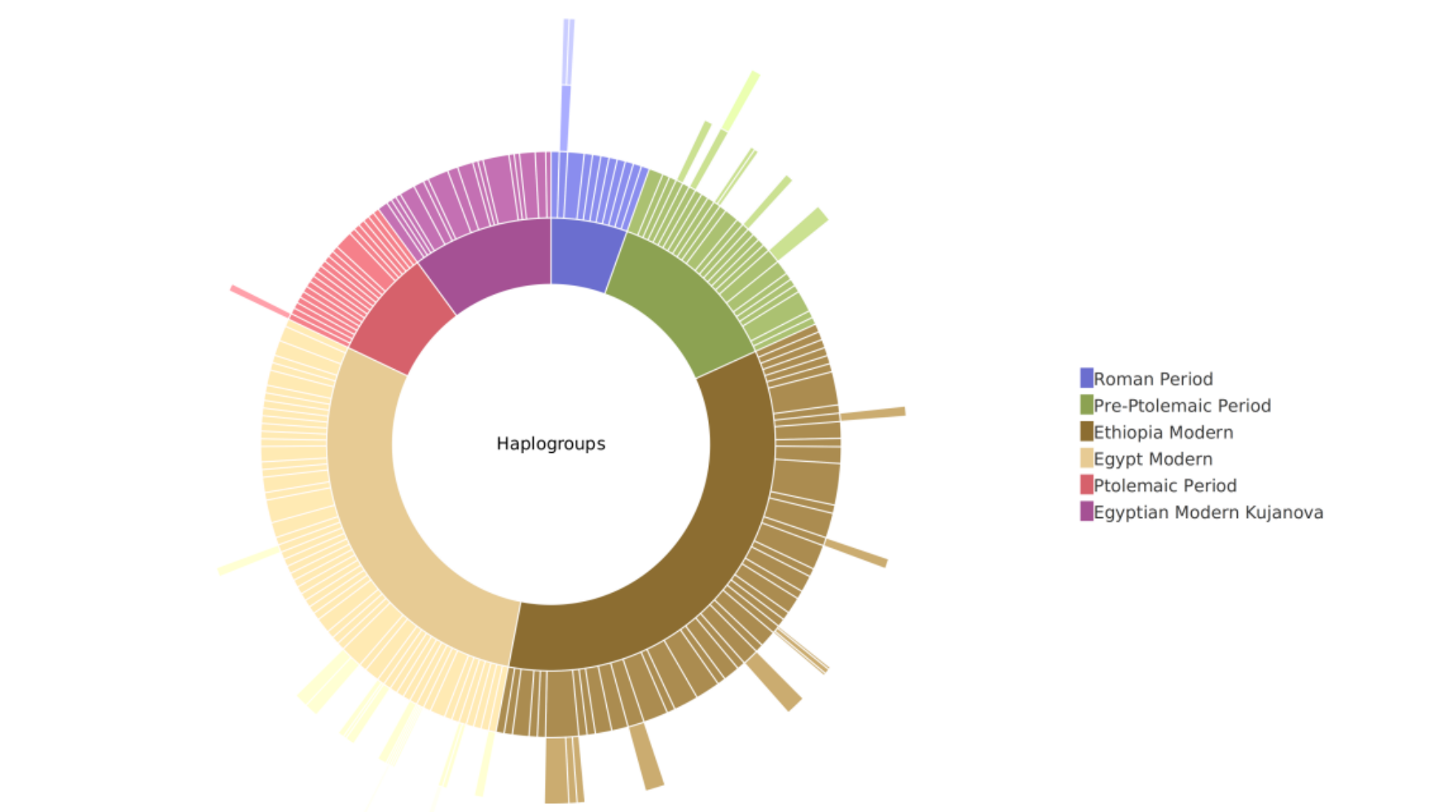
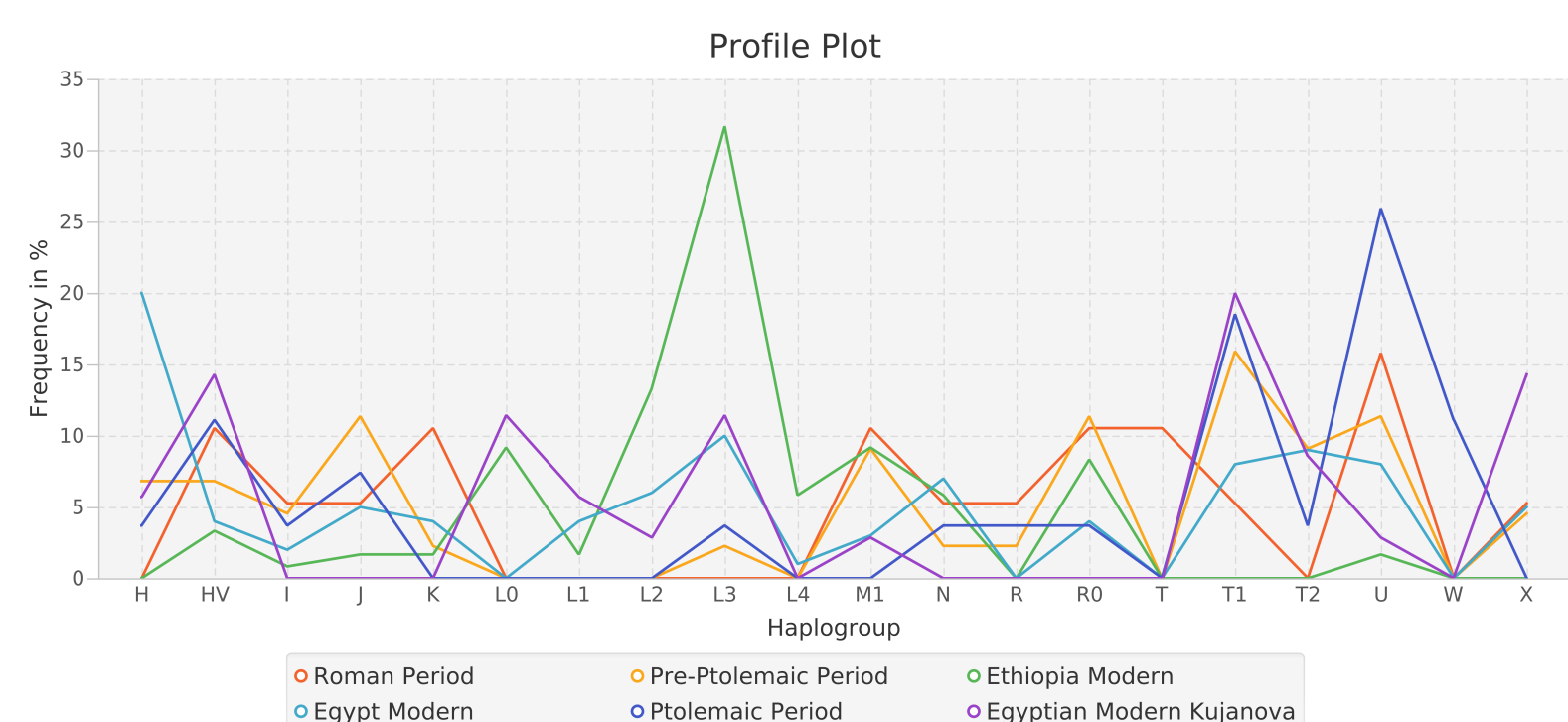
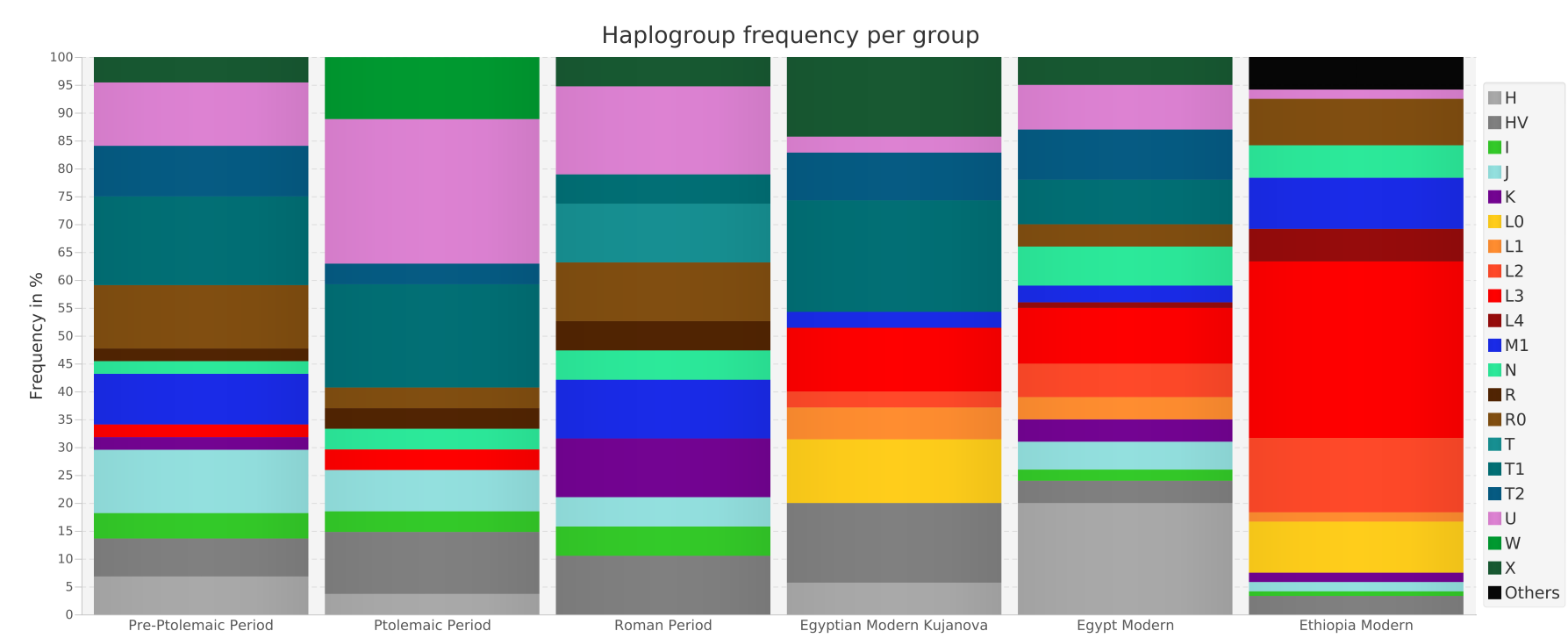
Data grouping

- interested in behaviour of different groups
→ Group data by feature
- internal grouping (columns not sorted)

Data filtering / Statistics

- Haplogroup filtering / frequencies
- Mutation filtering / frequencies

Data visualizations



MitoDB

- Web-Frontend with Vaadin Java Framework
- Backend with PostgreSQL, providing sequence information and meta-data (SQL)
- Curated data upload with metadata
- Retrieval possible through WebUI and mitoBench

Conclusion

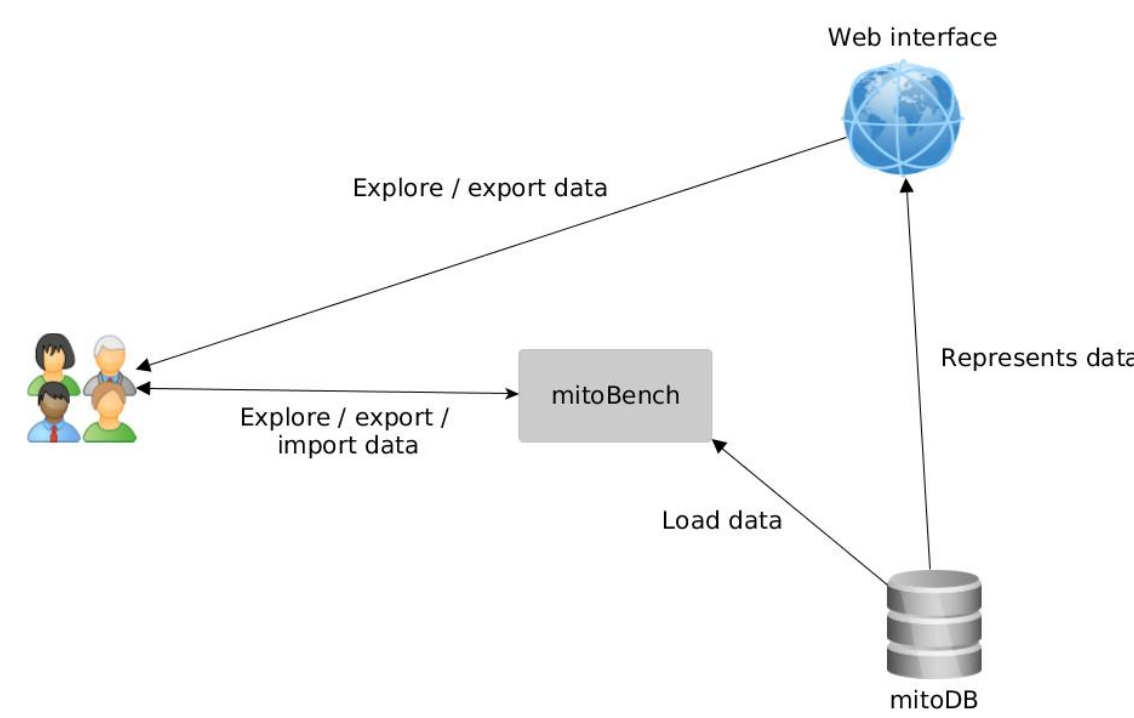
MitoBench

- Easy file handling and file conversion
- Combination, manipulation and visualization of mitochondrial data

- Data filtering
- Statistics

MitoDB

- Collection of mitochondrial data plus meta information
- Curated database
- accessible via mitoBench and web interface



References

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- Laurent Excoffier and Heidi EL Lischer. Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under linux and windows. *Molecular ecology resources*, 10(3):564-567, 2010.
- Hansi Weissensteiner, Dominic Pacher, Anita Kloss-Brandstätter, Lukas Forer, Günther Specht, Hans-Jürgen Bandelt, Florian Kronenberg, Antonio Salas, and Sebastian Schönherr. Haplogrep 2: mitochondrial haplogroup classification in the era of high-throughput sequencing. *Nucleic acids research*, page gkw233, 2016.

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